

```

TTGGGACCCAGCAGGACACAGCAGCAGTCAAGGTGCATGCTGGGACCGCGACGGACAGGCTGCCCGACCCCCAGGCCCCA 79
                                     M L A G G V R 7
BAGGCCAGTCTCTTTTCCCTCCCAACGCCCATCTGACCCAGGTGAGCAAGAGG ATG CTG GCG GGG GGC GTG AGG 151
S M P S P L L A C W Q P I L L L V L G S 27
AGC ATG CCC AGC CCC CTC CTG GCC TGC TGG CAG CCC ATC CTC CTG CTG GTG CTG GGC TCA 211
V L S G S A T G C P P R C E C S A Q D R 47
GTG CTG TCA GGC TCG GCC ACG GGC TGC CCG CCC CGC TGC GAG TGC TCC GCC CAG GAC CCG 271
A V L C H R K R F V A V P E G I P T E T 57
GCT GTG CTG TGC CAC CGC AAG CGC TTT GTG GCA GTC CCC GAG GGC ATC CCC ACC GAG ACG 331
R L L D L G K N R I K T L N Q D E F A S 37
CGC CTG CTG GAC CTA GGC AAG AAC CGC ATC AAA ACG CTC AAC CAG GAC GAG TTC GCC AGC 391
F P H L E E L E L N E N I V S A V E P G 107
TTC CCG CAC CTG GAG GAG CTG GAG CTC AAC GAG AAC ATC GTG AGC GCC GTG GAG CCC GGC 451
A F N N L F N L R T L G L R S N R L K L 127
GCC TTC AAC AAC CTC TTC AAC CTC CGG ACG CTG GGT CTC CGC AGC AAC CGC CTG AAG CTC 511
I P L G V F T G L S N L T K L D T R E N 147
ATC CCG CTA GGC GTC TTC ACT GGC CTC AGC AAC CTG ACC AAG CTG GAC ACG AGG GAG AAC 571
K I V I L L D Y M F Q D L Y N L K S L E 167
AAG ATC GTT ATC CTA CTG GAC TAC ATG TTT CAG GAC CTG TAC AAC CTC AAG TCA CTG GAG 631
V G D N D L V Y I S H R A F S G L N S L 187
GTT GGC GAC AAT GAC CTC GTC TAC ATC TCT CAC CGC GCC TTC AGC GGC CTC AAC AGC CTG 691
E Q L T L E K C N L T S I P T E A L S H 207
GAG CAG CTG ACT CTG GAG AAA TGC AAC CTG ACC TCC ATC CCC ACC GAG GCG CTG TCC CAC 751
L H G L I V L R L R H L N I N A I R D Y 227
CTG CAC GGC CTC ATC GTC CTG AGG CTC CGG CAC CTC AAC ATC AAT GCC ATC CGG GAC TAC 811
S F K R L Y R L K V L E I S H W P Y L D 247
TCC TTC AAG AGG CTG TAC CGA CTC AAG GTC TTG GAG ATC TCC CAC TGG CCC TAC TTG GAC 871
T M T P N C L Y G L N L T S L S I T H C 267
ACC ATG ACA CCC AAC TGC CTC TAC GGC CTC AAC CTG ACG TCC CTG TCC ATC ACA CAC TGC 931
N L T A V P Y L A V R H L V Y L R F L N 287
AAT CTG ACC GCT GTG CCC TAC CTG GCC GTC CGC CAC CTA GTC TAT CTC CGC TTC CTC AAC 991
L S Y N P I S T I E G S M L H E L L R L 307
CTC TCC TAC AAC CCC ATC AGC ACC ATT GAG GGC TCC ATG TTG CAT GAG CTG CTC CGG CTG 1051
Q E I Q L V G G Q L A V V E P Y A F R G 327
CAG GAG ATC CAG CTG GTG GGC GGG CAG CTG GCC GTG GTG GAG CCC TAT GCC TTC CGC GGC 1111
L N Y L R V L N V S G N Q L T T L E E S 347
CTC AAC TAC CTG CGC GTG CTC AAT GTC TCT GGC AAC CAG CTG ACC ACA CTG GAG GAA TCA 1171

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FIG. 1 (1 of 2)

**FIG. 1 (2 of 2)**

Input file T81; Output File T811.pat  
 Sequence length 979

	M	A	G	S	P	
GAATTCGGCAGGAGGCCAGCCAGTCCGCGCG/MCGRRGCCCGGCTCCCTGGGGCAGC	ATG	GCG	GGG	TGG	CCG	5
						72
L L W G :P R A G G V G L L V L L L L G L						25
CTG CTC TGG GGG CCG CCG GCC GGG GGC GTC GGC CTT TTG GTG CTG CTG CTG CTC GGC CTG						132
F R P P P A L C A R P V K E P R G L S A						45
TTT CCG CCG CCC CCC CCG CTC TGC GCG CCG CCG GTA AAG GAG CCC CCG GGC CTA AGC GCA						132
A S P P L A E T G A P R R F R R S V P R						65
GCG TCT CCG CCC TTG GCT GAG ACT GGC GCT CTT CCG CCG TTC CCG CCG TCA GTG CCC CGA						252
G E A A G A V Q E L A R A L A H L L E A						85
GGT GAG GCG GCG GGG GCG GTG CAG GAG CTG GCG CCG GCG CTG GCG CAT CTG CTG GAG GCC						312
E R Q E R A R A E A Q E A E D Q Q A R V						105
GAA COT CAG GAG CCG CCG CCG GCC GAG GCG CAG GAG GCT GAG GAT CAG CAG GCG CCG GTC						372
L A Q L L R V W G A P R N S D P A L G L						125
CTG GCG CAG CTG CTG CCG CTC TGG GCG GCG CCC CCG AAC TCT GAT CCG GCT CTG GCG TTG						432
D D D P D A P A A Q L A R A L L R A R L						145
GAC GAC GAC CCC GAC GCG CTT GCA GCG CAG CTC GCT CCG GCT CTG CTC CCG GCC CCG CTT						492
D P A A L A A Q L V P A P V P A A A L R						165
GAC CTT GCC GCC CTA GCA GCC CAG CTT GTG CCC GCG CCC GTC CCC GCC GCG GCG CTC CGA						552
P R P P V Y D D G P A G P D A E E A G D						185
CCC CCG CCC CCG GTC TAC GAC GAC GGC CCC GCG GGC CCG GAT GCT GAG GAG GCA GGC GAC						512
E T P D V D P E L L R Y L L G R I L A G						205
GAG ACA CCC GAC GTG GAC CCC GAG CTG TTG AGG TAC TTG CTG GGA CCG ATT CTT GCG GGA						672
S A D S E G V A A P R R L R R A A D H D						225
AGC GCG GAC TCC GAG GGG GTG GCA GCC CCG CCG CCG CTC CCG CGT GCC GCC GAC CAC GAT						732
V G S E L P P E G V L G A L L R V K R L						245
GTG GCG TCT GAG CTG CCC CTT GAG GGC GTG CTG GGG GCG CTG CTG CTT GTG AAA CCG CTA						792
E T P A P Q V P A R R L L P P *						261
GAG ACC CCG GCG CCC CAG GTG CTT GCA CCG CCG CTC TTG CCA CCC TGA						840
GCACTGCCCCGATCCCGTGACCCCTGGGACCCAGAGTGCCCCCGCCATCCCCGCCACGAGACTGCTCCCCGGCCAGCAC						919
GTCCAGAGCAACTTACCCCCGGCCAGCCAGCCCTCTCACCCGAGGATCCCTACCCCCCTGGC						979

FIG. 2

Fig 3

Σγ: 29.412

T79	1	MLAG	47
D45913	1	MARLSTGKAAC.QVVLGLLITSLTESSILTSECPLQCVCEIRPWF	44
T79	48	AVLCHRKRFVAVPEGIPTETRLDLGKNRIKTLNQDEFAS	87
D45913	45	TPQSTYREATTVDCNDLRLTRIPGNLSSDTQVLLLQSNNI	84
T79	88	FPHLEELNENIVSAVEPGAFFNLFNRLTLGLRSNRLKLIPLGVFTGLS	137
D45913	85	AKTVDELQQLFNLTEDFSQNNFTNIKEVGLANLT	119
T79	138	NLTKLDTRENNKIVILLDYMFDLYNLKSLEVGDNDLVYISHRAFSGLNSL	187
D45913	120	QLTTLHLEENQISEMTDYCLQDLNQLELYINHNNQISTISANAFSGLKNL	169
T79	188	EQLTLEKCNLTISIPTALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKV	237
D45913	170	LRLHLNSNKLKVIDSRWFDSTPNLEILMIGENFVIGILDMNFRPLSNLRS	219
T79	238	LEISHWPYLDTMTFNCLYGLN.LTSLSITHCNLTAVPYLAVRHLVYLRF	286
D45913	220	LVLG.MYLTDPGNALVGLDSLESLSFYDNKLIKVPQLALQKVPNLKFL	268
T79	287	NLSYNPISTIEGSMHELLRLQEIQLVG.GQLAVVEPY	323
D45913	269	DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELTKLE	318
T79	324	AFRGLNYLRLVNLVSGNQLTTLTEESVFHSGVGNLETLIL	360
D45913	319	ATNNPKLSYIHLAFRSVPALSLMLNNALNAVYQKTVESLPNLREISI	368
T79	361	DSNPLACDCRLLWVFRRLNLFNRQQPT.CATPEFVQGEKFDKDFPDVLL	409
D45913	369	HSNPLRCDCVIHWINSNKTNIREFMEPLSMFCAMPPEYRQQVK...EVLI	415
T79	410	PNYFT.CRRARIRDRKAQQVFVDEGHTVQFVCRADGDPPPAILWLSPRKH	458
D45913	416	QDSSEQCLPMISHDTFPNHLNMDIGTTFLDCRAMAEPEPEIYWVTPIGN	465
T79	459	LVSAKS.NGRLTVFPDGTLEVRYAQVQDNGTYLCIAANAGGNDSPAHLLH	507
D45913	466	KITVETLSDKYKLSSEGTLEIANIQIEDSGRYTCVAQNVOGADTRVATIK	515
T79	508	V.....RSYSPDWP HQ	518
D45913	516	VNGTLLDGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDN	565
T79	519	PNKTF.....AFISNQPGEGEANSTRA	540

**FIG. 3 (1 of 2)**

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D45913 566 PHITYTARVPVDVHEYNIHLQPSSTDYEVCLTVSNIHQQTQKSCVNVVTK 615
T79      541 TVPFPFDIKTLIIATTMGFI..SFLGVVLFCLVLLFLWSRGKGNTKHIE 588
D45913 616 TAAFALDISDHETSTALAAVMGSMFAVISLASIAIYIAKRFKRYHSL 665
T79      589 IEYVPRKSDAGISSADAPRKFNKMI..... 614
D45913 666 KKYMOKTSSIPLNEL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSYY 714

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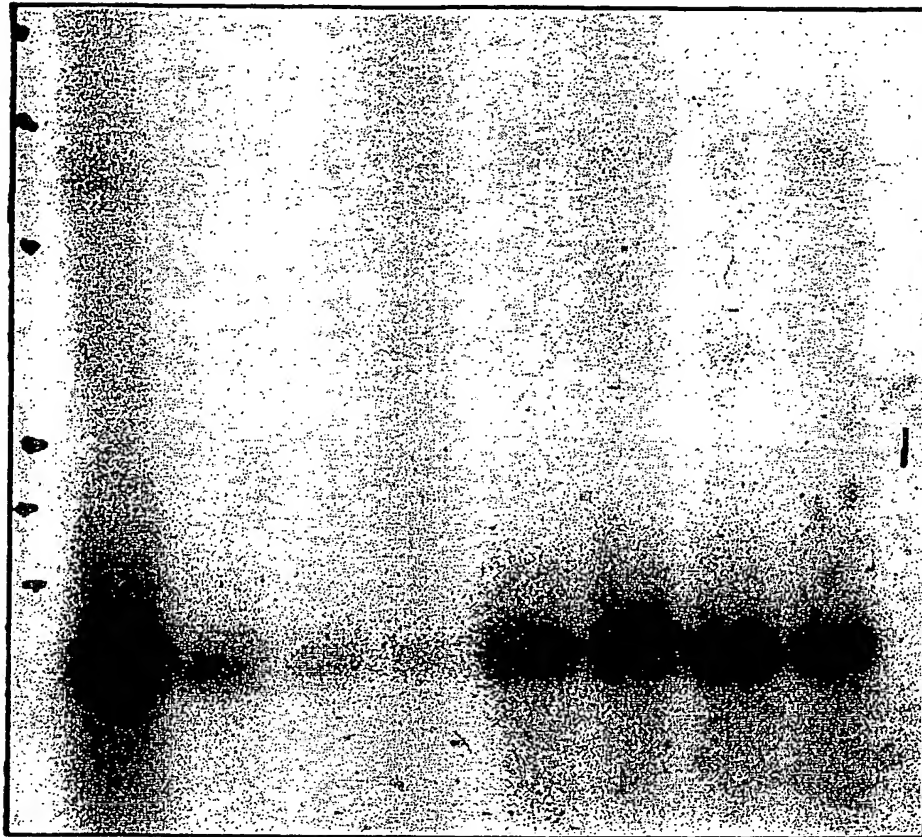


FIG. 4

T R P I L V I H D E Q K G P E V T S N	19
CC ACG COT CCG ATC TTG GTC ATC CAC GAT GAA CAG AAG GGG CCG GAA GTG ACC TCC AAT	59
A A L T L R N F C N W Q K Q H N P P S D	39
GCT GCC CTC ACT CTG CCG AAC TTT TGC AAC TGG CAG AAG CAG CAC AAC CCA CCC AGT GAC	119
R D A E H Y D T A I L F T R Q D L C G S	59
CCG GAT GCA GAG CAC TAT GAC ACA GCA ATT CTT TTC ACC AGA CAG GAC TTG TGT GGG TCC	179
Q T C D T L G M A D V G T V C D P S R S	79
CAG ACA TGT GAT ACT CTT GGG ATG GCT GAT GTT GGA ACT GTG TGT GAT CCG AGC AGA AGC	239
C S V I E D D G L Q A A F T T A H E L G	99
TGC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA GCC CAT GAA TTA GGC	299
H V F N M P H D D A K Q C A S L N G V N	119
CAC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CAG TGT GCC AGC CTT AAT GGT GTG AAC	359
Q D S H M M A S M L S N L D H S Q P W S	139
CAG GAT TCC CAC ATG ATG GCG TCA ATG CTT TCC AAC CTG GAC CAC AGC CAG CCT TGG TCT	419
P C S A Y M I T S F L D N G H G E C L M	159
CCT TCC AGT GCC TAC ATG ATT ACA TCA TTT CTG GAT AAT GGT CAT GGG GAA TGT TTG ATG	479
D K P Q N P I Q L P G D L P G T S Y D A	179
GAC AAG CCT CAG AAT CCC ATA CAG CTC CCA GGC GAT CTC CCT GGC ACC TCG TAC GAT GCC	539
N R Q C Q F T F G E D S K H C P D A A S	199
AAC CCG CAG TCC CAG TTT ACA TTT GGG GAG GAC TCC AAA CAC TCC CCT GAT GCA GCC AGC	599
T C S T L W C T G T S G G V L V C Q T K	219
ACA TGT AGC ACC TTG TGG TGT ACC GGC ACC TCT GGT GGG GTG CTG GTG TGT CAA ACC AAA	659
H F P W A D G T S C G E G K W C I N G K	239
CAC TTC CCG TGG GCG GAT GGC ACC AGC TGT GGA GAA GGG AAA TGG TGT ATC AAC GGC AAG	719
C V N K T D R K H F D T P F H G S W G M	259
TGT GTG AAC AAA ACC GAC AGA AAG CAT TTT GAT ACG CCT TTT CAT GGA AGC TGG GGA ATG	779
W G P W G D C S R T C G G G V Q Y T M R	279
TGG GGG CCT TGG GGA GAC TGT TCG AGA ACG TGC GGT GGA GGA GTC CAG TAC ACG ATG AGG	839
E C D N P V P K N G G K Y C E G K R V R	299
GAA TGT GAC AAC CCA GTC CCA AAG AAT GGA GGG AAG TAC TGT GAA GGC AAA CGA GTG CGC	899
Y R S C N L E D C P D N N G K T F R E E	319
TAC AGA TCC TGT AAC CTT GAG GAC TGT CCA GAC AAT AAT GGA AAA ACC TTT AGA GAG GAA	959
Q C E A H N E F S K A S F G S G P A V E	339
CAA TGT GAA GCA CAC AAC GAG TTT TCA AAA GCT TCC TTT GGG AGT GGG CCT GCG GTG GAA	1019
W I P K Y A G V S P K D R C K L I C Q A	359
TGG ATT CCC AAG TAC GCT GGC GTC TCA CCA AAG GAC AGG TGC AAG CTC ATC TGC CAA GCC	1079
K G I G Y F F V L Q P K V V D G T P C S	379
AAA GGC ATT GGC TAC TTC TTC GTT TTG CAG CCC AAG GTT GTA GAT GGT ACT CCA TGT AGC	1139

FIG. 5 (1 of 3)

P D S T S V C V Q G Q C V K A G C D R I	399
CCA GAT TCC ACC TCT GTC TGT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CCC ATC	1199
I D S K K K F D K C G V C G G N G S T C	419
ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TGC GGG GGA AAT GGA TCT ACT TGT	1259
K K I S G S V T S A K P G Y H D I I T I	439
AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT GGA TAT CAT GAT ATC ATC ACA ATT	1319
P T G A T N I E V K Q R N Q R G S R N N	459
CCA ACT GGA GCC ACC AAC ATC GAA GTG AAA CAG CGG AAC CAG AGG GGA TCC AGG AAC AAT	1379
G S F L A I K A A D G T Y I L N G D Y T	479
GGC AGC TTT CTT GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT	1439
L S T L E Q D I M Y K G V V L R Y S G S	499
TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG TAC AGC GGC TCC	1499
S A A L E R I R S F S P L K E P L T I Q	519
TCT GCG GCA TTG GAA AGA ATT CGC AGC TTT AGC CCT CTC AAA GAG CCC TTG ACC ATC CAG	1559
V L T V G N A L R P K I K Y T Y F V K K	539
GTT CTT ACT GTG GGC AAT GCC CTT CGA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG	1619
K K E S F N A I P T F S A W V I E E W G	559
AAG AAG GAA TCT TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC	1679
E C S K T C G K G Y K K R S L K C L S H	579
GAA TGT TCT AAG ACC TGT GCG AAG GGT TAC AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT	1739
D G G V L S H E S C D P L K K P K H F I	599
GAT GGA GGG GTG TTA TCT CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA	1799
D F C T M A E C S *	609
GAC TTT TGC ACA ATG GCA GAA TGC AGT TAA	1829
GTGGTTTAAGTGGTGTGTAGCTCTGAGGGCAAGGCAAGGTGAGGAAGGGCTGTGTCAGGGAAAGCAAGAAGGCTGGAGGG	1908
ATCCAGCGTATCTTGCAGTAACCACTGAGGTGTATCAGTAAGGTGGGATTATGGGGGTAGATAGAAAAGGAGTTGAAT	1987
CATCAGAGTAAACTGCCAGTTGCCAAATTTGATAGGATAGTTAGTGGAGGATTATTAACCTCTGAGCAGTGATATAGCATA	2066
ATAAAGCCCCGGGCAATTATTATTATTATTCTTTTGTGTACATCTATTACAAGTTTAGAAAAACAAGCAATTGTCPAA	2145
AAAAGTTAGAACTATTACAACCCCTGTTTCTGCTACTTATCAATACTTAGTATCATGGGGGTGGGAAATGAAAAGT	2224
AGGAGAAAAGTGAGATTTTACTAAGACCTGTTTACTTTACCTCACTAACAATGGGGGAGAAAGGAGTACAAATAGGA	2303
TCTTTGACCAGCACTGTTTATGGCTGCTATGGTTTCAGAGAATGTTTATACATTATTTCTACCGAGAATTAAACTTCA	2382
GATTGTTCAACATGAGAGAAAGGCTCAGCAACGTGAAATAACGCAATGGCTTCTCTTTCTTTTGGACCATCTCA	2461
GTCTTTATTTGTGTAAATTCATTTTGAGGAAAAACAACCTCCATGTATTTATTCAAGTGCAATTAAAGTCTACAATGGAAA	2540
AAAAGCAGTGAAGCATTAGATGCTGGTAAAGCTAGAGGAGACACAATGAGCTTAGTACCTCCAACCTCTCTTTTCC	2619
TACCATGTAACCTGCTTTGGGAATATGGATGTAAGAAGTAACCTTGTGTCTCATGAAAATCAGTACAATCACACAAGG	2698

FIG. 5 (2 of 3)



AGGATGAAACGCCCGAACAAAAATGAGGTGTGTAGAACAGGTTCCACAGGTTTGGGACATGAGATCACTTGTCTTC 2777  
TGGTGGGGAGGCTGCTGAGGGGTAGCAGGTCCATCTCCACAGCTGGTCCACAGTGGTATCCTGGTGAATGTCTCTTC 2856  
AGCTCTTTGTGTGAGAATATGATTTTTTCCATATGTATATAGTAAAAATATGTTACTATAAATTACATGTACTTTATAAGT 2935  
ATTGGTTTGGGTGTTCCTTCCAGAGGACTATAGTTAGTAATAAATGCCATATAAATACATATTTATTTTATACATTT 3014  
ATTTCTAATGAAAAAACTTTTAAATTATATCGCTTTTGTGGAAGTGCATATAAATAGAGTATTTATACAATATATGT 3093  
TACTAGAAATAAAAGAACACTTTTGGAAAAAAGGGCGGGCCGC 3147

TANGO 71/ADAMTS-1 Comparison (90% Protein Sequence Identity)

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251 DQSMADPHGSGLRHYLLTLFVVAARFYKHPSTIRNSISLVVVKILVTVEEQ 300
      |||||..||
1 .....TRPILVTHDEQ 11

301 KGFEVTSNAALTLRNFCSWQKQHNSPSDRDPEHYDTALLFTRODLGGSHT 350
      |||||..||
12 KGFEVTSNAALTLRNFCNWKQHNSPSDRDAEHYDTALLFTRODLGGSHT 61

351 CDTLGMADVGVTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKH 400
      |||||..||
62 CDTLGMADVGVTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQ 111

401 CASLNGVSGDSHLMASMLSSLDHSQFWSPCSAXMVTSLDNGHGECLMDK 450
      |||||..||
112 CASLNGVSNQDSHMMASMLSNLDHSQFWSPCSAXMVTSLDNGHGECLMDK 161

451 PQNPIRLPSDLPGTLYDANRQCQFTFGESKHCPLAASTCTTLWCITGTS 500
      |||||..||
162 PQNPIQLPGDLPGTLYDANRQCQFTFGESKHCPLAASTCTTLWCITGTS 211

501 GLLVCQTKHFPWADGTSCGEGKWCVSGRCVKNKIDKHFATPVHGSWGPWG 550
      |||||..||
212 GLLVCQTKHFPWADGTSCGEGKWCVSGRCVKNKIDKHFATPVHGSWGPWG 261

551 PWGDCSRTCCGGVQYTMRECIHFVFKNGGRYCEGRVRYRSCNIEDCPDN 600
      |||||..||
262 PWGDCSRTCCGGVQYTMRECIHFVFKNGGRYCEGRVRYRSCNIEDCPDN 311

601 NGKTFREEQCEAHNEFSKASFGNEPTVEWTPKYAGVSPKDRCKLTCEAKG 650
      |||||..||
312 NGKTFREEQCEAHNEFSKASFGSGFAVEWIPKYAGVSPKDRCKLTCEAKG 361

651 IGYFFVLQPKWVDGTPCSPDSTSVCVQGGCVKAGCDRIIDSKKKFDKGV 700
      |||||..||
362 IGYFFVLQPKWVDGTPCSPDSTSVCVQGGCVKAGCDRIIDSKKKFDKGV 411

701 CGGNGSTCKRMSGIVTSTRPGYHDIITIPAGATNIEVKHNRQGRSRNGS 750
      |||||..||
412 CGGNGSTCKRMSGIVTSTRPGYHDIITIPAGATNIEVKHNRQGRSRNGS 461

751 FLAIRAADGTYILNGNFTLSTLEQDLTYKGTVLRYSGSSAALERIRSFSP 800
      |||||..||
462 FLAIRAADGTYILNGNFTLSTLEQDLTYKGTVLRYSGSSAALERIRSFSP 511

801 LKEPLTIQVLNVGHALRPKIRFTYFMKKTESFNAIPTFSEWVIEEWGEC 850
      |||||..||
512 LKEPLTIQVLNVGHALRPKIRFTYFMKKTESFNAIPTFSAWVIEEWGE. 560

901 WSPCSRTCCGGVQYTMRECIHFVFKNGGRYCEGRVRYRSCNIEDCPDN 950
      |||||..||
561 ...CSKTCGGVQYTMRECIHFVFKNGGRYCEGRVRYRSCNIEDCPDN 607

951 S* 951
      |
608 S* 609

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FIG. 6

gtgcctac atg gtc acg tcc ttc cta gat aat gga cac ggg gaa tgt ttg 50  
Met Val Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu  
1 5 10

atg gac aag ccc cag aat cca atc aag ctc cct tct gat ctt ccc ggt 98  
Met Asp Lys Pro Gln Asn Pro Ile Lys Leu Pro Ser Asp Leu Pro Gly  
15 20 25 30

acc ttg tac gat gcc aac cgc cag tgt cag ttt aca ttc gga gag gaa 146  
Thr Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Glu  
35 40 45

tcc aag cac tgc cct gat gca gcc agc aca tgt act acc ctg tgg tgc 194  
Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Thr Thr Leu Trp Cys  
50 55 60

act ggc acc tcc ggt ggc tta ctg gtg tgc caa aca aaa cac ttc cct 242  
Thr Gly Thr Ser Gly Gly Leu Leu Val Cys Gln Thr Lys His Phe Pro  
65 70 75

tgg gca gat ggc acc agc tgt gga gaa ggg aag tgg tgt gtc agt ggc 290  
Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Val Ser Gly  
80 85 90

aag tgc gtg aac aag aca gac atg aag cat ttt gct act cct gtt cat 338  
Lys Cys Val Asn Lys Thr Asp Met Lys His Phe Ala Thr Pro Val His  
95 100 105 110

gga agc tgg gga cca tgg gga ccg tgg gga gac tgc tca aga acc tgt 386  
Gly Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys  
115 120 125

ggt ggt gga gtt caa tac aca atg aga gaa tgt gac aac cca gtc cca 434  
Gly Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro  
130 135 140

aag aac gga ggg aag tac tgt gaa ggc aaa cga gtc cgc tac agg tcc 482  
Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser  
145 150 155

tgt aac atc gag gac tgt cca gac aat aac gga aaa acg ttc aga gag 530  
Cys Asn Ile Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu  
160 165 170

gag cag tgc gag gcg cac aat gag ttt tcc aaa gct tcc ttt ggg aat 578  
Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Asn  
175 180 185 190

gag ccc act gta gag tgg aca ccc aag tac gcc ggc gtc tcg cca aag 626  
Glu Pro Thr Val Glu Trp Thr Pro Lys Tyr Ala Gly Val Ser Pro Lys  
195 200 205

Fig. 7 (1 of 4)

gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc	674
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe	
210 215 220	
gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct	722
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser	
225 230 235	
acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc	770
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg	
240 245 250	
atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga	818
Ile Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly	
255 260 265 270	
aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga	866
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg	
275 280 285	
cct ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att	914
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile	
290 295 300	
gaa gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt	962
Glu Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe	
305 310 315	
ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc	1010
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe	
320 325 330	
act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta	1058
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu	
335 340 345 350	
agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt	1106
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser	
355 360 365	
cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct	1154
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala	
370 375 380	
ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aag aca gag	1202
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu	
385 390 395	
tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg	1250
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp	
400 405 410	

Fig. 7 (2 of 4)

ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtg	1298
Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val	
115 420 425 430	
cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa	1346
Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu	
435 440 445	
gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac	1394
Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His	
450 455 460	
tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt	1442
Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly	
465 470 475	
tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta	1490
Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu	
480 485 490	
tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac	1538
Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp	
495 500 505 510	
ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg	1592
Phe Cys Thr Leu Thr Gln Cys Ser	
515	
ggaggggctg atacactgag tgcaagagta ctggagggat ccagtgagtc aaaccagtaa	1652
gcagtgaggt gtggcaagga ggtgtgtgta ggggatacat agcaaaggag gtagatcagg	1712
acactaccct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa	1772
gaccatacag agcactaagg agcccccagg cactattagt atctcttttc ttatatctat	1832
cgcccaaata attttcagag tctggcagaa gccctgttgc actgtactaa ctagatactt	1892
cttatcacaa agattgggaa aggcaaagca gaaagatggg aagactgggt ttcaaacaag	1952
gcttggtttc aatcactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc	2012
gctgggtgct gtggttttac ggaaggttga tgcattcatt ctatcaacag tgaaaagttc	2072
agcttggtca acgtgacaga aaggctcatc tccgtgaaaag agctcctgat ttcttcttac	2132
accatctcag ttcttaacta tagttcatgt tgaggtagaa acaattcatc tattttataaa	2192
atgtacattg gaaaaaaaaa gtgaagttta tgaggtagac ataaaaactg aaggaaacaa	2252
tgagcaacat gcctcctgct ttgcttcctc ctgaggtaaa cctgcctggg gattgagggt	2312
gtttaagatt atccatggct cacaagaggc agtaaaataa tacatgttgt gccagagtta	2372
gaatggggta tagagatcag ggtcccatga gatggggaac atggtgatca ctcatctcac	2432
atgggaggct gctgcagggt agcagggtcca ctccctggcag ctggtccaac agtcgtatcc	2492
tggtgaatgt ctgttcagct cttctactga gagagaatat gactgtttcc atatgtatat	2552
gtatatagta aaatatgtta ctatgaattg catgtacttt ataagtattg gtgtgtctgt	2612
tccttctaag aaggactata gtttataata aatgcctata ataacatatt tatttttata	2672
cattttatttc taatgataaa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa	2732
atagagtatt tataacaatat atgttaacta gaaataataa aagaacactt ttgaatgtgt	2792
atgcctattt tctggagtgg gattaacttc tgggcaagaa atctgatgag acacaaacat	2852
tggacttcaa gacagtttta aattttgggt aaatgaactg tatttcctgt ttatagacgt	2912
actaataaaa aagaagttag tgatgtcttt agtggttaaga ttgttactaa tgtggttggc	2972
aaattgctgt aaagagccag atagtaagca tttatggcat tgtaggctat ctttcctgcc	3032
acaaccatgt gacagtgagt gctttgtagg actgagagca gccataaatg acatgtaaat	3092

Fig. 7 (3 of 4)

gataaactgt ggctgtgctt taataaaact ttatttacaa aaaaaaaaaa aaa

3145

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gcggccgctc ccggccggcc caagggacag agccaggctc cgggagcccg caacactcgt 60
cctgagagcc ccggctcctc agcccgtac ggccagggcc tcggcctccg cccccgactc 120
ccgagctcct gccctagagt cgactgggct cccgcccgcg tgggacagac agacggagac 180
ccagccctgc gagggcgcg cgaccgggcg gaggtgttgt aggaggagac cgaggagggg 240
ggctgggctg gggctggggc cgcgccggca agagagacat gcgattggtg accaagccga 300
gcggacggac agcgcgccc ag atg cag gtg agc gag agg atg ctg gca ggg 352
                               Met Gln Val Ser Glu Arg Met Leu Ala Gly
                               1           5           10

ggt atg aga agc atg ccc agc ccc ctc ctg gcc tgc tgg cag ccc atc 400
Gly Met Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile
                               15           20           25

ctc ctg ctg gta ctg ggc tca gtg ctg tca ggc tct gct aca ggc tgc 448
Leu Leu Leu Val Leu Gly Ser Val Leu Ser Gly Ser Ala Thr Gly Cys
                               30           35           40

ccg ccc cgc tgc gag tgc tca gcg cag gac cga gcc gtg ctc tgc cac 496
Pro Pro Arg Cys Glu Cys Ser Ala Gln Asp Arg Ala Val Leu Cys His
                               45           50           55

cgc aaa cgc ttt gtg gcg gtg ccc gag ggc atc ccc acc gag act cgc 544
Arg Lys Arg Phe Val Ala Val Pro Glu Gly Ile Pro Thr Glu Thr Arg
                               60           65           70

ctg ctg gac ctg ggc aaa aac cgc atc aag aca ctc aac cag gac gag 592
Leu Leu Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu
                               75           80           85           90

ttt gcc agc ttc cca cac ctg gag gag cta gaa ctc aat gaa aac atc 640
Phe Ala Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile
                               95           100           105

gtg agc gcc gtg gag cca ggc gcc ttc aac aac ctc ttc aac ctg agg 688
Val Ser Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg
                               110           115           120

act ctg ggg ctg cgc agc aac cgc ctg aag ctt atc ccg ctg ggc gtc 736
Thr Leu Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro Leu Gly Val
                               125           130           135

ttc acc ggc ctc agc aac ttg acc aag ctg gac atc agt gag aac aag 784
Phe Thr Gly Leu Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys
                               140           145           150

atc gtc atc ctg cta gac tac atg ttc caa gac cta tac aac ctc aag 832
Ile Val Ile Leu Leu Asp Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys
                               155           160           165           170

tcg ctg gag gtc ggc gac aac gac ctc gtc tac atc tcc cat cga gcc 880
Ser Leu Glu Val Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala
                               175           180           185

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Fig. 8 (1 f 2)

ttc agc ggc ctc aac agc ctg gaa cag ctg acg ctg gag aaa tgc aat	928
Phe Ser Gly Leu Asn Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn	
190 195 200	
ctg acc tcc atc ccc acg gag gcg ctc tcc cac ctg cac ggc ctc atc	976
Leu Thr Ser Ile Pro Thr Glu Ala Leu Ser His Leu His Gly Leu Ile	
205 210 215	
gtc ctg cgg cta cga cat ctc aac atc aat gcc atc agg gac tac tcc	1024
Val Leu Arg Leu Arg His Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser	
220 225 230	
ttc aag agg ctg tac cga ctt aag gtc tta gag atc tcc cac tgg ccc	1072
Phe Lys Arg Leu Tyr Arg Leu Lys Val Leu Glu Ile Ser His Trp Pro	
235 240 245 250	
tac ctg gac acc ata acc ccc cgg acg cgt ggg tcg ac	1110
Tyr Leu Asp Thr Ile Thr Pro Arg Thr Arg Gly Ser	
255 260	



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ctcctggatg tgcgcagccg cagagcgctg ctgctgtgcc taatacccat cgctgcgcac 60
ttgacagcca gtccgcccgt ccggagcccc gctcgttggg gcagc atg gcg ggg tcg 117
                                     Met Ala Gly Ser
                                     1

ccg ctg ctc tgc ggg ccg cgg gcc ggg ggc gtc ggc att ttg gtg ctg 165
Pro Leu Leu Cys Gly Pro Arg Ala Gly Gly Val Gly Ile Leu Val Leu
  5                      10                      15                      20

ctg ctc ttg ggc ctt ctg agg ctg ccc ccc acc ctg tca gcg agg ccc 213
Leu Leu Leu Gly Leu Leu Arg Leu Pro Pro Thr Leu Ser Ala Arg Pro
      25                      30                      35

gtg aag gag ccc cgc agt ctg agc gca gca tcc gcg ccc ttg gtt gag 261
Val Lys Glu Pro Arg Ser Leu Ser Ala Ala Ser Ala Pro Leu Val Glu
      40                      45                      50

acg agc act ccc ctc cgc ttg cgt cgg gcc gtg ccc cga gga gag gcg 309
Thr Ser Thr Pro Leu Arg Leu Arg Arg Ala Val Pro Arg Gly Glu Ala
      55                      60                      65

gcg ggt gcg gtg cag gag ctg gcg cgg gcg ctg gcg cac ctg ctg gag 357
Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu Leu Glu
      70                      75                      80

gcc gag aga cag gaa cgc gcg cgt gct gag gcg cag gag gct gag gat 405
Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala Glu Asp
      85                      90                      95                      100

cag cag gcg cgt gtc ctg gcg cag ctg ctg cgc gcc tgg ggc tct ccg 453
Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Ala Trp Gly Ser Pro
      105                      110                      115

cgt gcc tcg gac ccg ccc ttg gcc ccc gac gat gac ccg gac gct cca 501
Arg Ala Ser Asp Pro Pro Leu Ala Pro Asp Asp Asp Pro Asp Ala Pro
      120                      125                      130

gct gca cag ctc gcc cgt gct ctg ctc cga gct cgc cta gac ccc ggc 549
Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp Pro Gly
      135                      140                      145

ccc cag tgt atg atg atg gcc cca ctg gcc cag acg tcg agg atg ccg 597
Pro Gln Cys Met Met Met Ala Pro Leu Ala Gln Thr Ser Arg Met Pro
      150                      155                      160

gcg acg aga ctc ctg acg tgg acc ctg agc tgc tgaggtactt gctagggcgg 650
Ala Thr Arg Leu Leu Thr Trp Thr Leu Ser Cys
      165                      170                      175

atcctcaccg gaagttcgga gccagaggct gctcctgccc cgcgcgcgct ccgccgatct 710
gtggaccagg atttgggtcc cgaggtgccc cctgagaacg tactgggggc tctgctacgc 770
gtcaaacgcc tggagaaccc ctgcgccag gcgcgggcac gccgcctcct gcctccctga 830

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Fig. 9 (1 of 2)

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gcgotgctgc atcctgcacg ccttgaacc caggagcgcc ccagcaaccc tgactccctg 890
ccagcacgtc caaggctgct taccacagca acctccatc cctgagccc tcaataaatg 950
ccatctgtag caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1010
aaaaaaaaaa aaaaaaa                                     1027
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